

Supplementary table 1 Sample IDs for transcriptome sequencing

Sample ID	RNA integrity	Concen. (ng/ul)	Raw Reads	Clean reads	Clean bases (G)	Error (%)	Q20 (%)	Q30 (%)	GC (%)
	number (RIN)								
HH1_N1	9.3	414	84746676	82076208	12.3	0.03	96.85	92.17	58.14
HH1_N2	7.6	252	91823824	89358204	13.4	0.03	97.2	93.01	58.02
HS1_N1	8.4	1455	87533090	84776044	12.72	0.03	96.44	91.23	58.13
HS1_N2	7.8	1986	80827066	78473126	11.77	0.03	95.92	90.09	57
HH1_Y1	8.6	324	78351662	76208670	11.43	0.03	97.01	92.49	57.67
HH1_Y2	8.4	416	83163428	80515340	12.08	0.03	97	92.5	58.74
HH1_Y3	8.9	674	91357512	88846572	13.33	0.03	97.3	93.23	58.61
HS1_Y1	8.9	1290	97436460	94259192	14.14	0.03	96.46	91.35	58.29
HS1_Y2	8.6	1350	92684804	89648842	13.45	0.03	96.4	91.22	58.46
HS1_Y3	6.6	90	86012194	84258058	12.64	0.03	97.05	92.27	49.4
HH5_1	8.3	134	81247180	78253286	11.74	0.03	97.3	93.26	59.02
HH5_2	9.5	42	92765874	90002040	13.5	0.03	96.84	92.14	54.7
HH5_3	7.8	338	87389764	84746764	12.71	0.03	97.1	92.81	58.38
HS5_1	8.8	204	100102332	97325590	14.6	0.03	96.42	91.29	58.04
HS5_2	7.1	204	98119576	95197288	14.28	0.03	96.36	91.15	56.88
HS5_3	6.4	78	87681000	84955022	12.74	0.03	96.35	91.06	55.88

Supplementary table 2 Summary of primers of real-time PCR assay

Gene ID	Symbol	Primer-F (5'-3')	Primer-R (3'-5')
Cluster-33503.52810	ARRB	AAAACAGAAAGGGAAACG	AGGAGGTGGGCGAAGA
XM_007527837.2	GAPDH	ACTCCAATCACGGCAAAT	GTACTCGGCACCAGCATC
Cluster-33503.134689	GRB2	GGGGTTTGATGCGGATAT	GCCACCGAAAGTGACGAG
Cluster-33503.28078	HOXC13	GTGACCCTGGAGCAAA	CTATCTATTAGTGGGACTTGG
Cluster-33503.122683	KRT1	AGCCGCAGTTGCCACA	CCAGCACGATGCCTTACA
Cluster-33503.128985	LEF1	TTCCCGTAGTTGTCCCG	TGAATGCGTTCATGCTGT
Cluster-33503.47741	RSPO2	CCGGAGACCCTGGAGTTGT	GGACCGCCAGAGGCAATT
Cluster-33503.95190	SFN	CTCACTTCACAGAGCCTTTC	GCTGCTGCGAGACAACCT
Cluster-33503.30444	TCF7	CAAAGTGATTGCCGAGTG	TTGTCCCGTGCTGACC
Cluster-33503.107807	TCNNB1	CTTCTGGGCTACGATGAC	CAACTCTGCTTCCTGGTG
Cluster-33503.38152	TGFB2	GAACCCGACTGTGCTGA	TGCTCCGTCCTCTTTA
Cluster-33503.47776	WIF1	AAGTTCGTCTGTAGCGTGAT	CCTTCTCCAATGTTCCCT

Supplementary table 3 Differentially expressed genes between HS1N and HS1Y

Gene ID	HS1N_readcount	HS1Y_readcount	log2FoldChange	p-value	padj
Cluster-33503.128444	0	86.08214993	-21.625	9.31E-07	0.010868
Cluster-33503.125788	0	63.24402852	-21.197	1.52E-06	0.016849
Cluster-33503.71896	0	30.45082855	-20.179	4.74E-06	0.036887
Cluster-33503.160189	0	43.12854788	-7.8749	2.08E-06	0.020771
Cluster-33503.115414	1.453397872	57.98866115	-5.2885	2.29E-06	0.021883
Cluster-33503.50680	21.81424054	336.6388061	-3.9508	5.45E-10	1.64E-05
Cluster-33503.127585	42.52858859	558.0876554	-3.7159	2.27E-11	7.94E-07
Cluster-33503.89984	96.11450522	896.5460164	-3.2208	4.10E-06	0.034448
Cluster-33503.121879	25.91251299	236.8442846	-3.1921	7.28E-07	0.009559
Cluster-82032.0	18.83532828	172.1416422	-3.1884	9.18E-07	0.010868
Cluster-33503.129745	160.6011264	1414.024237	-3.1376	7.34E-09	0.000141
Cluster-33503.40595	11872.35656	2226.207379	2.4149	1.77E-06	0.018626
Cluster-33503.107453	4977.639861	896.6663599	2.4726	3.93E-06	0.034428
Cluster-33503.30824	514.2493259	71.4815556	2.8474	5.04E-06	0.03779
Cluster-33503.86800	9843.401602	1356.213765	2.8594	4.34E-06	0.035042
Cluster-33503.64008	192.0790232	19.91437288	3.2642	2.88E-07	0.004321
Cluster-33503.107454	7002.950394	673.0459194	3.3788	2.45E-09	5.72E-05
Cluster-33503.84059	409.0755235	25.82116204	3.9892	3.70E-12	1.56E-07
Cluster-33503.40525	90.36019879	4.296914424	4.4067	4.09E-07	0.005723
Cluster-33503.69414	1973.58419	87.84111687	4.4903	7.56E-20	5.29E-15
Cluster-33503.93070	30.37756328	0	7.4075	2.73E-06	0.024973
Cluster-33503.71791	1155.372535	5.005001278	7.8257	2.25E-32	2.36E-27
Cluster-33503.74871	2263.274482	6.711504128	8.3611	3.22E-39	6.77E-34
Cluster-33503.93079	135.0359235	0	9.5605	1.45E-12	7.61E-08
Cluster-33503.43551	188.7802277	0	24.007	2.92E-08	0.000472
Cluster-33503.96104	289.6354178	0	24.591	1.34E-08	0.000234
Cluster-33503.78173	398.7659056	0	25.028	7.37E-09	0.000141
Cluster-33503.83755	1125.957687	0	26.444	9.97E-10	2.62E-05

Supplementary table 4 Differentially expressed genes between HH1N and HH1Y

Gene ID	HH1N_readcount	HH1Y_readcount	log2FoldChange	pval	padj
Cluster-33503.110885	0	66.63694	-21.368	1.25E-06	0.004152
Cluster-24458.2	0	32.18077	-20.354	3.92E-06	0.010497
Cluster-33503.125440	0	55.892	-20.339	3.96E-06	0.010497
Cluster-33503.27650	0	31.01105	-20.297	4.17E-06	0.010871
Cluster-33503.71896	0	30.28986	-20.271	4.29E-06	0.011009
Cluster-23971.0	0	35.42226	-7.6936	1.78E-06	0.005659
Cluster-50926.0	0.901617	96.81909	-6.71	1.04E-08	6.86E-05
Cluster-33503.28873	1.381753	62.27404	-5.4875	3.64E-06	0.009968
Cluster-33503.115414	6.575269	120.4126	-4.202	5.87E-10	5.19E-06
Cluster-33503.52438	22.75327	396.6611	-4.1295	1.07E-12	2.43E-08
Cluster-33503.45503	6.967422	111.498	-4.001	3.33E-09	2.52E-05
Cluster-33503.50611	18.53091	272.9855	-3.88	2.69E-13	7.12E-09
Cluster-27220.0	3.606467	53.88451	-3.878	2.76E-06	0.007966
Cluster-33503.93776	12.19027	163.9718	-3.7533	8.46E-12	1.22E-07
Cluster-33503.50604	8.349175	99.9293	-3.5813	6.44E-08	0.000301
Cluster-33503.50610	18.13876	206.5931	-3.5106	5.67E-10	5.19E-06
Cluster-33503.48696	6.428629	71.85253	-3.4766	1.35E-06	0.004382
Cluster-33503.50609	238.1785	2496.305	-3.3895	7.59E-14	2.41E-09
Cluster-33503.63866	11.34731	114.1013	-3.3365	1.05E-07	0.000453
Cluster-33503.50605	102.2464	946.8086	-3.2117	2.29E-11	2.80E-07
Cluster-33503.50612	53.87748	491.173	-3.1887	2.24E-10	2.54E-06
Cluster-33503.50603	127.7263	1118.064	-3.13	2.65E-12	4.22E-08
Cluster-33503.142390	14.18035	109.9152	-2.9497	1.15E-05	0.025082
Cluster-33503.46837	15.73808	116.9022	-2.8927	1.83E-06	0.005715
Cluster-33503.38566	49.4976	350.2752	-2.8215	2.98E-10	3.16E-06
Cluster-33503.99443	30.35835	203.1055	-2.7441	1.26E-07	0.000526
Cluster-33503.121879	55.20058	369.5113	-2.7422	1.25E-12	2.49E-08
Cluster-33503.83099	17.86392	118.1429	-2.7299	3.00E-06	0.008518
Cluster-33503.82604	17.11983	106.4645	-2.6336	2.53E-06	0.007435
Cluster-33503.99455	29.61426	168.1658	-2.5049	3.03E-07	0.001203
Cluster-33503.98985	10642.13	58233.13	-2.452	2.11E-12	3.73E-08
Cluster-33503.67947	46.9285	245.385	-2.388	3.29E-07	0.001276
Cluster-33503.29591	103.148	535.5993	-2.3771	7.70E-06	0.018372
Cluster-33503.99442	159.3264	820.5364	-2.3635	1.25E-06	0.004152
Cluster-33503.99447	226.9377	1160.856	-2.3547	5.41E-09	3.74E-05
Cluster-33503.54524	329.2436	1651.53	-2.3271	3.89E-08	0.000221
Cluster-33503.74547	71.06352	343.8941	-2.2767	6.33E-06	0.01572
Cluster-33503.50680	106.0984	468.9649	-2.1445	2.40E-08	0.000147
Cluster-33503.127585	171.9499	758.9011	-2.1422	6.02E-08	0.000293
Cluster-33503.142217	362.7567	1510.353	-2.0577	4.61E-09	3.33E-05
Cluster-33503.65963	183.4179	728.9146	-1.9904	5.16E-08	0.000274
Cluster-33503.146366	64.33406	253.8232	-1.9797	2.11E-05	0.042495

Cluster-33503.47433	139.3853	547.822	-1.9753	5.97E-08	0.000293
Cluster-33503.82343	95.15411	364.9328	-1.9382	7.03E-07	0.002523
Cluster-33503.30717	139.8437	531.9532	-1.9288	1.10E-05	0.024208
Cluster-33503.72876	1685.051	6280.95	-1.8983	1.87E-07	0.000761
Cluster-33503.67786	388.3833	1446.21	-1.8967	6.09E-08	0.000293
Cluster-33503.29548	300.8745	1092.506	-1.8604	5.04E-07	0.001906
Cluster-33503.99017	840.049	3018.019	-1.8451	4.64E-08	0.000254
Cluster-33503.99433	1030.144	3678.842	-1.8364	4.84E-06	0.012221
Cluster-33503.100134	453.1346	1589.09	-1.8099	9.05E-06	0.02084
Cluster-33503.27620	91.22503	317.2852	-1.7969	9.81E-06	0.021966
Cluster-33503.98980	508.7717	1736.197	-1.7707	7.04E-08	0.000319
Cluster-33503.99016	629.7241	2135.446	-1.7615	8.88E-07	0.003069
Cluster-33503.93217	493.6202	1591.578	-1.6888	6.43E-06	0.015728
Cluster-33503.122220	386.1359	1220.254	-1.6596	7.75E-06	0.018372
Cluster-33503.101049	103.639	326.9984	-1.6574	1.72E-05	0.035084
Cluster-33503.50332	712.5724	2184.052	-1.616	1.24E-05	0.025979
Cluster-33503.46860	1229.407	3761.834	-1.6134	3.36E-06	0.009362
Cluster-33503.46861	216.9503	662.6814	-1.6107	2.16E-05	0.042999
Cluster-33503.100489	129.951	380.4445	-1.5494	2.36E-05	0.045818
Cluster-33503.93054	676.0603	1952.662	-1.5302	2.47E-06	0.007404
Cluster-33503.75382	939.2504	317.2232	1.5656	9.69E-06	0.021966
Cluster-33503.35295	356.3305	83.65786	2.092	2.22E-05	0.043585
Cluster-33503.78577	239.3139	42.47672	2.4952	1.21E-05	0.025556
Cluster-33503.33273	576.0719	93.63076	2.6223	8.61E-06	0.020121
Cluster-33503.27714	180.362	25.62775	2.8089	1.57E-05	0.032501
Cluster-33503.40311	7501.224	1055.103	2.8298	1.35E-11	1.79E-07
Cluster-33503.35715	124.3904	16.40437	2.9238	1.21E-05	0.025556
Cluster-33503.76770	95.66024	10.65527	3.1688	5.44E-07	0.002011
Cluster-33503.84059	323.3889	18.92224	4.0987	4.40E-17	1.75E-12
Cluster-33503.69414	1457.644	82.54651	4.1441	4.51E-22	2.39E-17
Cluster-33503.93079	64.05922	0.682505	6.5507	8.67E-08	0.000383
Cluster-33503.114665	111.8005	1.026904	6.7686	7.14E-07	0.002523
Cluster-33503.85379	99.62864	0.701846	7.1757	1.90E-06	0.005821
Cluster-33503.71791	710.5572	2.449937	8.2083	1.22E-33	1.94E-28
Cluster-33503.74871	1137.66	0.721187	10.697	1.26E-22	9.98E-18
Cluster-33503.95063	186.6346	0	23.912	3.31E-08	0.000195
Cluster-33503.96104	259.6656	0	24.361	1.82E-08	0.000116
Cluster-33503.78173	795.2259	0	25.776	2.59E-09	2.06E-05
Cluster-33503.103697	1325.376	0	26.565	8.36E-10	7.00E-06
Cluster-33503.83755	1722.539	0	26.949	4.77E-10	4.74E-06

Supplementary table 5 NCBI accession numbers of *KRT1* sequences from 19 species

Species	NCBI accession number
<i>Erinaceus europaeus</i>	XM_007535509.2
<i>Odobenus rosmarus</i>	XM_004410492.1
<i>Ursus arctos</i>	XM_026491053.1
<i>Ursus maritimus</i>	XM_008701257.1
<i>Ailuropoda melanoleuca</i>	XM_011228597.2
<i>Canis lupus</i>	XM_025440552.1
<i>Vulpes vulpes</i>	XM_025987081.1
<i>Mustela putorius</i>	XM_004772755.2
<i>Rousettus aegyptiacus</i>	XM_016150993.1
<i>Equus asinus</i>	XM_014833554.1
<i>Callorhinus ursinus</i>	XM_025861805.1
<i>Condylura cristata</i>	XM_004684201.2
<i>Lontra canadensis</i>	XM_032871791.1
<i>Phoca vitulina</i>	XM_032396498.1
<i>Zalophus californianus</i>	>XM_027625808.1
<i>Felis catus</i>	XM_006940344.3
<i>Tupaia chinensis</i>	XM_006155972.3
<i>Trichechus manatus</i>	XM_004390333.2
<i>Callithrix jacchus</i>	XM_002748619.3